

<120> DcR3 Polypeptide, A TNFR Homolog

<160> 18

09896096.062801

Cys	Asn	Val	Leu	Cys	Gly	Glu	Arg	Glu	Glu	Glu	Ala	Arg	Ala	Cys	95	100	105
His	Ala	Thr	His	Asn	Arg	Ala	Cys	Arg	Cys	Arg	Thr	Gly	Phe	Phe	110	115	120
Ala	His	Ala	Gly	Phe	Cys	Leu	Glu	His	Ala	Ser	Cys	Pro	Pro	Gly	125	130	135
Ala	Gly	Val	Ile	Ala	Pro	Gly	Thr	Pro	Ser	Gln	Asn	Thr	Gln	Cys	140	145	150
Gln	Pro	Cys	Pro	Pro	Gly	Thr	Phe	Ser	Ala	Ser	Ser	Ser	Ser	Ser	155	160	165
Glu	Gln	Cys	Gln	Pro	His	Arg	Asn	Cys	Thr	Ala	Leu	Gly	Leu	Ala	170	175	180
Leu	Asn	Val	Pro	Gly	Ser	Ser	Ser	His	Asp	Thr	Leu	Cys	Thr	Ser	185	190	195
Cys	Thr	Gly	Phe	Pro	Leu	Ser	Thr	Arg	Val	Pro	Gly	Ala	Glu	Glu	200	205	210
Cys	Glu	Arg	Ala	Val	Ile	Asp	Phe	Val	Ala	Phe	Gln	Asp	Ile	Ser	215	220	225
Ile	Lys	Arg	Leu	Gln	Arg	Leu	Leu	Gln	Ala	Leu	Glu	Ala	Pro	Glu	230	235	240
Gly	Trp	Gly	Pro	Thr	Pro	Arg	Ala	Gly	Arg	Ala	Ala	Leu	Gln	Leu	245	250	255
Lys	Leu	Arg	Arg	Arg	Leu	Thr	Glu	Leu	Leu	Gly	Ala	Gln	Asp	Gly	260	265	270
Ala	Leu	Leu	Val	Arg	Leu	Leu	Gln	Ala	Leu	Arg	Val	Ala	Arg	Met	275	280	285
Pro	Gly	Leu	Glu	Arg	Ser	Val	Arg	Glu	Arg	Phe	Leu	Pro	Val	His	290	295	300

<210> 2
 <211> 1114
 <212> DNA
 <213> Homo sapiens

<220>
 <221> Unsure
 <222> 1090

<223> Unknown base

<400> 2

tccgcaggcg gaccgggggc aaaggaggtg gcatgtcggc caggcacagc 50
agggctctgt gtccgcgctg agccgcgctc tccctgctcc agcaaggacc 100
atgagggcgc tggagggggc aggcctgtcg ctgctgtgcc tgggtgttggc 150
gctgcctgcc ctgctgccgg tgccggctgt acgcggagtg gcagaaacac 200
ccacctaccc ctggcgggac gcagagacag gggagcggct ggtgtgcgcc 250
cagtgcctcc caggcacctt tgtgcagcgg ccgtgccgcc gagacagccc 300
cacgacgtgt ggcccgtgtc caccgcgcca ctacacgcag ttctggaact 350
acctggagcg ctgccgtac tgcaacgtcc tctgcgggga gcgtgaggag 400
gaggcacggg cttgccacgc caccacaac cgtgcctgcc gctgccgcac 450
cggtctcttc gcgcacgtg gtttctgctt ggagcacgca tcgtgtccac 500
ctggtgccgg cgtgattgcc ccgggcaccc ccagccagaa cacgcagtgc 550
cagccgtgcc cccaggcac cttctcagcc agcagctcca gctcagagca 600
gtgccagccc caccgcaact gcacggccct gggcctggcc ctcaatgtgc 650
caggctcttc ctccatgac accctgtgca ccagctgcac tggttcccc 700
ctcagcacca gggtaaccagg agctgaggag tgtgagcgtg ccgtcatcga 750
ctttgtggct ttccaggaca tctccatcaa gaggtgcag cggtgctgc 800
agggcctcga gggcccggag ggctggggtc cgacaccaag ggccggccgc 850
gcggccttgc agctgaagct gcgtcggcgg ctcacggagc tcctgggggc 900
gcaggacggg gcgtgctgg tgccgctgct gcaggcgtg cgcgtggcca 950
ggatgcccgg gctggagcgg agcgtccgtg agcgttccct ccctgtgcac 1000
tgatcctggc cccctcttat ttattctaca tccttggcac cccacttgca 1050
ctgaaagagg ctttttttta aatagaagaa atgaggtttn ttaaaaaaaaa 1100
aaaaaaaaaa aaaa 1114

<210> 3

<211> 491

05996096-062801

<212> DNA
<213> Unknown

<220>
<223> Unknown organism

<220>
<221> unsure
<222> 62, 73, 86, 98
<223> unknown base

<400> 3
gccgagacag cccacgacg tgtggcccgt gtccaccgcg ccactacacg 50
cagttctgga antaactgga gcnctgccgc tactgnaacg tcctctgngg 100
ggagcgtgag gaggaggcac gggcttgcca cgccaccac aaccgtgcct 150
gccgctgccg caccggcttc ttcgcgcacg ctggtttctg cttggagcac 200
gcatcgtgtc cacctggtgc cggcgtgatt gccccgggca cccccagcca 250
gaacacgcag tgcctagccg tgccccccag gcaccttctc agccagcagc 300
tccagctcag agcagtgcc accccaccgc aactgcacgg ccctgggcct 350
ggccctcaat gtgccaggct ctctctccca tgacaccctg tgcaccagct 400
gcactggctt cccctcagc accagggtag caggagctga ggagtgtgag 450
cgtgccgtca tcgactttgt ggctttccag gacatctcca t 491

<210> 4
<211> 73
<212> DNA
<213> Unknown

<220>
<223> Unknown organism

<400> 4
gccgagacag cccacgacg tgtggcccgt gtccaccgcg ccactacacg 50
cattctggaa ctacctggag cgc 73

<210> 5
<211> 271
<212> DNA
<213> Unknown

<220>

<220>
<221> unsure
<222> 142
<223> unknown base

<400> 7
gaggggcccc caggagtggg ggccggaggt gtggcagggg tcaggttgct 50
ggccccagcc ttgcacctg agctaggaca ccagttcccc tgacctgtt 100
cttccctcct ggctgcaggc acccccagcc agaacacgca gnccagccgt 150
gccccccagg cacctttctca gccagcagct ccagctcaga gcagtgccag 200
ccccaccgca actgcacggc cctggggcctg gccctcaatg tgccaggctc 250
ttcctcccat gacacctgt gcaccag 277

<210> 8
<211> 199
<212> DNA
<213> Unknown

<220>
<223> Unknown organism

<400> 8
gcacgtgtc cacctggtgc eggcgtgatt gcccgggca ccccagcca 50
gaacacgcag gcttagccgt gccccccagg cacctttctca gccagcagct 100
ccagctcaga gcagtgccag cccccaccgca actgcacggc cctggggcctg 150
gccctcaatg tgccaggctc ttcctcccat gacacctgt gcaccagct 199

<210> 9
<211> 226
<212> DNA
<213> Unknown

<220>
<223> Unknown organism

<220>
<221> unsure
<222> 4, 9, 12, 165
<223> unknown base

<400> 9
agcngtgcnc cncaggcacc ttctcagcca gcagttccag ctcagagcag 50

tgccagcccc accgcaactg caccggccctg ggccctggccc tcaatgtgcc 100
 aggtctttcc tcccatgaca cgctgtgcac cagctgcact ggcttcccc 150
 tcagcaccag ggtancagga gctgaggagt gtgagcgtgc cgtcacgcac 200
 tttgtggctt tccaggacat ctccat 226

<210> 10
 <211> 283
 <212> DNA
 <213> Homo sapiens

<220>
 <221> Unsure
 <222> 1-283
 <223> Unknown organism

<220>
 <221> unsure
 <222> 27, 64, 140
 <223> unknown base

<400> 10
 cttgtccacc tgggtgccgc gtgattnccc gggcaccccc agccagaaca 50
 cgcagtgccg gccntcccc caggcacctt ctcagccagc agctccagct 100
 cagagcagtg ccagccccac cgcaactgca acgccctggn ctggccctca 150
 atgtgccagg ctcttctctc catgacaccc tgtgcaccag ctgcactggc 200
 ttccccctca gcaccagggg accaggagct gaggagtgtg agcgtgccgt 250
 catcgacttt gtggctttcc aggacatctc cat 283

<210> 11
 <211> 21
 <212> DNA
 <213> Unknown

<220>
 <223> Unknown organism

<400> 11
 cacgctgggt tctgcttgga g 21

<210> 12
 <211> 22
 <212> DNA

<213> Unknown

<220>

<223> Unknown organism

<400> 12

agctggtgca caggggtgtca tg 22

<210> 13

<211> 53

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<400> 13

cccaggcacc ttctcagcca gccagcagct ccagctcaga gcagtgccag 50

ccc 53

<210> 14

<211> 24

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<400> 14

acacgatgcg tgctccaagc agaa 24

<210> 15

<211> 17

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<400> 15

cttcttcgcg cacgctg 17

<210> 16

<211> 16

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<400> 16
atcacgcccgg caccag 16

<210> 17
<211> 461
<212> PRT
<213> Homo sapiens

<400> 17
Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu
1 5 10 15
Leu Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr
20 25 30
Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr
35 40 45
Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly
50 55 60
Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys
65 70 75
Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val
80 85 90
Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln Val
95 100 105
Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys Thr Cys
110 115 120
Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys Arg
125 130 135
Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala
140 145 150
Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala
155 160 165
Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg
170 175 180
Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser
185 190 195
Arg Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala
200 205 210

09896096 "052301

05896096 "062301

Pro Gly Ala Val	His Leu Pro Gln Pro	Val Ser Thr Arg Ser	Gln
	215	220	225
His Thr Gln Pro	Thr Pro Glu Pro Ser	Thr Ala Pro Ser Thr	Ser
	230	235	240
Phe Leu Leu Pro	Met Gly Pro Ser Pro	Pro Ala Glu Gly Ser	Thr
	245	250	255
Gly Asp Phe Ala	Leu Pro Val Gly Leu	Ile Val Gly Val Thr	Ala
	260	265	270
Leu Gly Leu Leu	Ile Ile Gly Val Val	Asn Cys Val Ile Met	Thr
	275	280	285
Gln Val Lys Lys	Lys Pro Leu Cys Leu	Gln Arg Glu Ala Lys	Val
	290	295	300
Pro His Leu Pro	Ala Asp Lys Ala Arg	Gly Thr Gln Gly Pro	Glu
	305	310	315
Gln Gln His Leu	Leu Ile Thr Ala Pro	Ser Ser Ser Ser Ser	Ser
	320	325	330
Leu Glu Ser Ser	Ala Ser Ala Leu Asp	Arg Arg Ala Pro Thr	Arg
	335	340	345
Asn Gln Pro Gln	Ala Pro Gly Val Glu	Ala Ser Gly Ala Gly	Glu
	350	355	360
Ala Arg Ala Ser	Thr Gly Ser Ser Asp	Ser Ser Pro Gly Gly	His
	365	370	375
Gly Thr Gln Val	Asn Val Thr Cys Ile	Val Asn Val Cys Ser	Ser
	380	385	390
Ser Asp His Ser	Ser Gln Cys Ser Ser	Gln Ala Ser Ser Thr	Met
	395	400	405
Gly Asp Thr Asp	Ser Ser Pro Ser Glu	Ser Pro Lys Asp Glu	Gln
	410	415	420
Val Pro Phe Ser	Lys Glu Glu Cys Ala	Phe Arg Ser Gln Leu	Glu
	425	430	435
Thr Pro Glu Thr	Leu Leu Gly Ser Thr	Glu Glu Lys Pro Leu	Pro
	440	445	450
Leu Gly Val Pro	Asp Ala Gly Met Lys	Pro Ser	
	455	460	

<210> 18
 <211> 293
 <212> PRT
 <213> Homo sapiens

<400> 18

Met	Asn	Lys	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser	
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Ile	Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His	
				20					25					30	
Tyr	Asp	Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro	
				35					40					45	
Pro	Gly	Thr	Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr	
				50					55					60	
Val	Cys	Ala	Pro	Cys	Pro	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	His	
				65					70					75	
Thr	Ser	Asp	Glu	Cys	Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu	
				80					85					90	
Gln	Tyr	Val	Lys	Gln	Glu	Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys	
				95					100					105	
Glu	Cys	Lys	Glu	Gly	Arg	Tyr	Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys	
				110					115					120	
His	Arg	Ser	Cys	Pro	Pro	Gly	Phe	Gly	Val	Val	Gln	Ala	Gly	Thr	
				125					130					135	
Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Arg	Cys	Pro	Asp	Gly	Phe	Phe	
				140					145					150	
Ser	Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys	Arg	Lys	His	Thr	Asn	
				155					160					165	
Cys	Ser	Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys	Gly	Asn	Ala	Thr	
				170					175					180	
His	Asp	Asn	Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr	Gln	Lys	Cys	
				185					190					195	
Gly	Ile	Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg	Phe	Ala	
				200					205					210	
Val	Pro	Thr	Lys	Phe	Thr	Pro	Asn	Trp	Leu	Ser	Val	Leu	Val	Asp	
				215					220					225	

09896096-063001

Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
 230 235 240

Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys
 245 250 255

Leu Trp Lys His Gln Asn Lys Ala Gln Asp Ile Val Lys Lys Ile
 260 265 270

Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile
 275 280 285

Gly His Ala Asn Leu Thr Phe Glu
 290

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